

OIPE

## RAW SEQUENCE LISTING

DATE: 06/15/2001

PATENT APPLICATION: US/09/865,993

TIME: 16:54:46

Input Set : A:\RTS-0175 Sequence Listing.txt

Output Set: N:\CRF3\06152001\I865993.raw

Does Not Comply  
Corrected Diskette Needed

6 <110> APPLICANT: Brett P. Monia  
 7 Andrew T. Watt  
 9 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 5  
 EXPRESSION

11 <130> FILE REFERENCE: RTS-0175  
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/865,993  
 C--> 13 <141> CURRENT FILING DATE: 2001-05-25  
 13 <160> NUMBER OF SEQ ID NOS: 89  
 16 <210> SEQ ID NO: 1  
 17 <211> LENGTH: 20  
 18 <212> TYPE: DNA  
 19 <213> ORGANISM: Artificial Sequence  
 21 <220> FEATURE:  
 23 <223> OTHER INFORMATION: Antisense Oligonucleotide  
 25 <400> SEQUENCE: 1  
 26 tccgtcatcg ctccctcaggg 20  
 29 <210> SEQ ID NO: 2  
 30 <211> LENGTH: 20  
 31 <212> TYPE: DNA  
 32 <213> ORGANISM: Artificial Sequence  
 34 <220> FEATURE:  
 36 <223> OTHER INFORMATION: Antisense Oligonucleotide  
 38 <400> SEQUENCE: 2  
 39 atgcattctg cccccaagga 20  
 42 <210> SEQ ID NO: 3  
 43 <211> LENGTH: 2139  
 44 <212> TYPE: DNA  
 45 <213> ORGANISM: Homo sapiens  
 47 <220> FEATURE:  
 49 <220> FEATURE:  
 50 <221> NAME/KEY: CDS  
 51 <222> LOCATION: (47)...(1201)  
 53 <400> SEQUENCE: 3  
 54 cgcggggcgc gcggcgcggg gcggcctggc cggcggcggc ggcggc atg aag gtc 55  
 55 Met Lys Val  
 56 1  
 58 acg tcg ctc gac ggg cgc cag ctg cgc aag atg ctc cgc aag gag gcg 103  
 59 Thr Ser Leu Asp Gly Arg Gln Leu Arg Lys Met Leu Arg Lys Glu Ala  
 60 5 10 15  
 62 gcg gcg cgc tgc gtg gtg ctc gac tgc cgg ccc tat ctg gcc ttc gct 151  
 63 Ala Ala Arg Cys Val Val Leu Asp Cys Arg Pro Tyr Leu Ala Phe Ala  
 64 20 25 30 35  
 66 gcc tcg aac gtg cgc ggc tcg ctc aac gtc aac ctc aac tcg gtg gtg 199  
 67 Ala Ser Asn Val Arg Gly Ser Leu Asn Val Asn Leu Asn Ser Val Val  
 68 40 45 50  
 70 ctg cgg cgg gcc cgg ggc ggc gcg gtg tcg gcg cgc tac gtg ctg ccc 247  
 71 Leu Arg Arg Ala Arg Gly Gly Ala Val Ser Ala Arg Tyr Val Leu Pro  
 72 55 60 65

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74	gac gag gcg gcg cgc gcg cgg ctc ctg cag gag ggc ggc ggc ggc gtc	295
75	Asp Glu Ala Ala Arg Ala Arg Leu Leu Gln Glu Gly Gly Gly Gly Val	
76	70 75 80	
78	gcg gcc gtg gtg gtg ctg gac cag ggc agc cgc cac tgg cag aag ctg	343
79	Ala Ala Val Val Val Leu Asp Gln Gly Ser Arg His Trp Gln Lys Leu	
80	85 90 95	
82	cga gag gag agc gcc gcg cgt gtc gtc ctc acc tcg cta ctc gct tgc	391
83	Arg Glu Glu Ser Ala Ala Arg Val Val Leu Thr Ser Leu Leu Ala Cys	
84	100 105 110 115	
86	cta ccc gcc ggc ccg cgg gtc tac ttc ctc aaa ggg gga tat gag act	439
87	Leu Pro Ala Gly Pro Arg Val Tyr Phe Leu Lys Gly Gly Tyr Glu Thr	
88	120 125 130	
90	ttc tac tcg gaa tat cct gag tgt tgc gtg gat gta aaa ccc att tca	487
91	Phe Tyr Ser Glu Tyr Pro Glu Cys Cys Val Asp Val Lys Pro Ile Ser	
92	135 140 145	
94	caa gag aag att gag agt gag aga gcc ctc atc agc cag tgt gga aaa	535
95	Gln Glu Lys Ile Glu Ser Glu Arg Ala Leu Ile Ser Gln Cys Gly Lys	
96	150 155 160	
98	cca gtg gta aat gtc agc tac agg cca gct tat gac cag ggt ggc cca	583
99	Pro Val Val Asn Val Ser Tyr Arg Pro Ala Tyr Asp Gln Gly Gly Pro	
100	165 170 175	
102	gtt gaa atc ctt ccc ttc ctc tac ctt gga agt gcc tac cat gca tcc	631
103	Val Glu Ile Leu Pro Phe Leu Tyr Leu Gly Ser Ala Tyr His Ala Ser	
104	180 185 190 195	
106	aag tgc gag ttc ctc gcc aac ttg cac atc aca gcc ctg ctg aat gtc	679
107	Lys Cys Glu Phe Leu Ala Asn Leu His Ile Thr Ala Leu Leu Asn Val	
108	200 205 210	
110	tcc cga cgg acc tcc gag gcc tgc atg acc cac cta cac tac aaa tgg	727
111	Ser Arg Arg Thr Ser Glu Ala Cys Met Thr His Leu His Tyr Lys Trp	
112	215 220 225	
114	atc cct gtg gaa gac agc cac acg gct gac att agc tcc cac ttt caa	775
115	Ile Pro Val Glu Asp Ser His Thr Ala Asp Ile Ser Ser His Phe Gln	
116	230 235 240	
118	gaa gca ata gac ttc att gac tgt gtc agg gaa aag gga ggc aag gtc	823
119	Glu Ala Ile Asp Phe Ile Asp Cys Val Arg Glu Lys Gly Gly Lys Val	
120	245 250 255	
122	ctg gtc cac tgt gag gct ggg atc tcc cgt tca ccc acc atc tgc atg	871
123	Leu Val His Cys Glu Ala Gly Ile Ser Arg Ser Pro Thr Ile Cys Met	
124	260 265 270 275	
126	gct tac ctt atg aag acc aag cag ttc cgc ctg aag gag gcc ttc gat	919
127	Ala Tyr Leu Met Lys Thr Lys Gln Phe Arg Leu Lys Glu Ala Phe Asp	
128	280 285 290	
130	tac atc aag cag agg agg agc atg gtc tcg ccc aac ttt ggc ttc atg	967
131	Tyr Ile Lys Gln Arg Arg Ser Met Val Ser Pro Asn Phe Gly Phe Met	
132	295 300 305	
134	ggc cag ctc ctg cag tac gaa tct gag atc ctg ccc tcc acg ccc aac	1015
135	Gly Gln Leu Leu Gln Tyr Glu Ser Glu Ile Leu Pro Ser Thr Pro Asn	
136	310 315 320	
138	ccc cag cct ccc tcc tgc caa ggg gag gca gca ggc tct tca ctg ata	1063

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139 Pro Gln Pro Pro Ser Cys Gln Gly Glu Ala Ala Gly Ser Ser Leu Ile
140      325                      330                      335
142 ggc cat ttg cag aca ctg agc cct gac atg cag ggt gcc tac tgc aca      1111
143 Gly His Leu Gln Thr Leu Ser Pro Asp Met Gln Gly Ala Tyr Cys Thr
144 340                      345                      350                      355
146 ttc cct gcc tcg gtg ctg gca ccg gtg cct acc cac tca aca gtc tca      1159
147 Phe Pro Ala Ser Val Leu Ala Pro Val Pro Thr His Ser Thr Val Ser
148                      360                      365                      370
150 gag ctc agc aga agc cct gtg gca acg gcc aca tcc tgc taa aactgggatg 1211
151 Glu Leu Ser Arg Ser Pro Val Ala Thr Ala Thr Ser Cys
W--> 152      375                      380                      385
154 gaggaatcgg ccagccccca agagcaactg tgatttttgt ttttaagact catggacatt 1271
156 tcataacctga tgcaatactg aagacctcat tctgtcatgc tgccccagtg agatagtgag 1331
158 tggtcaccag gcttgcaaat gaacttcaga cggacctcag ggtaggttct cgggactgaa 1391
160 ggaaggccaa gccattacgg gagcacagca tgtgctgact actgtacttc cagaccctg 1451
162 ccctcttggg actgccaggt ccttgcaact cagagtctgc cttttcattt caagcataag 1511
164 gcaataaata cctgcagcaa cgtgggagaa agaagttgct ggaccaggag aaaaggcagt 1571
166 tatgaagcca attcattttg aaggaagcac aatttccacc ttattttttg aactttggca 1631
168 gtttcaatgt ctgtctctgt tgcttcgggg cataagctga tcaccgtcta gttgggaaag 1691
170 taacctaca gggttttag ggacatgatc agcatcctga tttgaaccct gaaatgttgt 1751
172 gtagacaccc tttgggtcc aatgaggtag ttgggtgaag tagcaagatg ttggcttttc 1811
174 tggatttttt ttgccatggg ttcttctactg accttggaact ttggcatgat tcttagtcat 1871
176 acttgaactt gtctcattcc acctcttctc agagcaactc ttcctttggg aaaagagttc 1931
178 ttcagatcat agacaaaaaa agtcatacct tgcaggtggt agcagtagat tccaggagga 1991
180 gaagggtact tgctaggtat cctgggtcag tggcggtgca aactggtttc ctcagctgcc 2051
182 tgtccttctg tgtgcttatg tctcttgatg caattgtttt cctccctgcc cctggaggtt 2111
184 gtcttcaagc tgtggacttc tgggattt      2139
187 <210> SEQ ID NO: 4
188 <211> LENGTH: 24
189 <212> TYPE: DNA
190 <213> ORGANISM: Artificial Sequence
192 <220> FEATURE:
194 <223> OTHER INFORMATION: PCR Primer
196 <400> SEQUENCE: 4
197 tgacccacct acactacaaa tgga      24
200 <210> SEQ ID NO: 5
201 <211> LENGTH: 25
202 <212> TYPE: DNA
203 <213> ORGANISM: Artificial Sequence
205 <220> FEATURE:
207 <223> OTHER INFORMATION: PCR Primer
209 <400> SEQUENCE: 5
210 cttcttgaaa gtgggagcta atgtc      25
213 <210> SEQ ID NO: 6
214 <211> LENGTH: 23
215 <212> TYPE: DNA
216 <213> ORGANISM: Artificial Sequence
218 <220> FEATURE:
220 <223> OTHER INFORMATION: PCR Probe

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222 <400> SEQUENCE: 6
223 cctgtggaag acagccacac ggc                                     23
226 <210> SEQ ID NO: 7
227 <211> LENGTH: 19
228 <212> TYPE: DNA
229 <213> ORGANISM: Artificial Sequence
231 <220> FEATURE:
233 <223> OTHER INFORMATION: PCR Primer
235 <400> SEQUENCE: 7
236 gaaggtgaag gtcggagtc                                     19
239 <210> SEQ ID NO: 8
240 <211> LENGTH: 20
241 <212> TYPE: DNA
242 <213> ORGANISM: Artificial Sequence
244 <220> FEATURE:
246 <223> OTHER INFORMATION: PCR Primer
248 <400> SEQUENCE: 8
249 gaagatggtg atgggatttc                                     20
252 <210> SEQ ID NO: 9
253 <211> LENGTH: 20
254 <212> TYPE: DNA
255 <213> ORGANISM: Artificial Sequence
257 <220> FEATURE:
259 <223> OTHER INFORMATION: PCR Probe
261 <400> SEQUENCE: 9
262 caagcttccc gttctcagcc                                     20
265 <210> SEQ ID NO: 10
266 <211> LENGTH: 2479
267 <212> TYPE: DNA
268 <213> ORGANISM: Homo sapiens
270 <220> FEATURE:
273 <400> SEQUENCE: 10
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276 tgcgcgcgccc ctcgggcgcc gggctccgtc gcggccgcag ccccgcggtg cgccctcccg    120
278 tgccctgccc gcggacaccc tggccgtgga caccctggcc gtgggcaccc gcggggcgcg    180
280 cggcgcgggg cgctggccg gcggcgcgcg cggcatgaag gtcacgtcgc tcgacgggcg    240
282 ccagctgcgc aagatgctcc gcaaggaggg ggcgcgcgcg tgcgtggtgc tcgactgccg    300
284 gccctatctg gccttcgctg cctcgaacgt gcgcggctcg ctcaacgtca acctcaactc    360
286 ggtggtgctg cggcgggccc gggcgggcgc ggtgtcggcg cgctacgtgc tgcccagcga    420
288 ggcggcgcgc gcgcggctcc tgcaggaggg cggcgggcgc gtcgcggccg tgggtggtgct    480
290 ggaccagggc agccgccact ggcagaagct gcgagaggag agcgccgcgc gtgtcgtcct    540
292 cacctcgcta ctcgcttgcc taccgcggcg cccgcgggtc tacttctcta aagggggata    600
294 tgagactttc tactcggaat atcctgagtg ttgcgtggat gtaaaaccca ttccacaaga    660
296 gaagattgag agtgagagag ccctcatcag ccagtgtgga aaaccagtgg taaatgtcag    720
298 ctacaggcca gcttatgacc aggggtggccc agttgaaatc cttcccttcc tctaccttgg    780
300 aagtgcctac catgcatcca agtgcgagtt cctcgccaac ttgcacatca cagccctgct    840
302 gaatgtctcc cgacggacct ccgaggcctg catgaccacac ctacactaca aatggatccc    900
304 tgtggaagac agccacacgg ctgacattag ctcccacttt caagaagcaa tagacttcat    960
306 tgactgtgtc agggaaaagg gaggcaaggt cctggtccac tgtgaggctg ggatctcccc   1020

```

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```

308 ttcacccacc atctgcatgg cttacotttat gaagaccaag cagttccgcc tgaaggaggc 1080
310 cttcgattac atcaagcaga ggaggagcat ggtctcgccc aactttggct tcatgggcca 1140
312 gctcctgcag tacgaatctg agatcctgcc ctccacgccc aacccccagc ctccctcctg 1200
314 ccaaggggag gcagcaggct cttcactgat aggccatttg cagacactga gccctgacat 1260
316 gcagggtgcc tactgcacat tccctgcctc ggtgctggca cgggtgccta cccactcaac 1320
318 agtctcagag ctacgcagaa gccctgtggc aacggccaca tctgctaaa actgggatgg 1380
320 aggaatcggc ccagcccca gagcaactgt gatttttgtt ttttaagactc atggacattt 1440
322 catacctgat gcaatactga agacctcatt ctgtcatgct gccccagtga gatagtgagt 1500
324 ggtcaccagg cttgcaaatg aacttcagac ggacctcagg gtaggttctc gggactgaag 1560
326 gaaggccaag ccattacggg agcacagcat gtgctgacta ctgtacttcc agaccctgc 1620
328 cctcttggga ctgcccagtc cttgcacctc agagttcgcc ttttcatttc aagcataagg 1680
330 caataaatac ctgcagcaac gtgggagaaa gaagttgctg gaccaggaga aaaggcagtt 1740
332 atgaagccaa ttcattttga aggaagcaca atttccacct tattttttga actttggcag 1800
334 tttcaatgtc tgtctctgtt gcttcggggc ataagctgat caccgtctag ttgggaaagt 1860
336 aacctacag ggtttgtagg gacatgatca gcactctgat ttgaaccctg aaatgttgtg 1920
338 tagacacct cttgggtcca atgaggtagt tgggtgaagt agcaagatgt tggcttttct 1980
340 ggattttttt tgccatgggt tcttactga ccttggactt tggcatgatt cttagtata 2040
342 cttgaacttg tctcattcca cctcttctca gagcaactct tcccttggga aaagagttct 2100
344 tcagatcata gacaaaaaaa gtcatacctt cgaggtggta gcagtagatt ccaggaggag 2160
346 aagggtactt gctaggtatc ctgggtcagt ggcggtgcaa actggtttcc tcagctgcct 2220
348 gtcttctgt gtgcttatgt ctcttctgac aattgttttc ctccctgcc ctggagggtg 2280
350 tcttcaagct gtggacttct gggatttgca gattttgcaa cgtggtacta ctttttttcc 2340
352 tttttgtctg ttagttattt ctccagggga aaaggcaata attttctaag acccgtgtga 2400
354 atgtgaagaa aagcagtatg ttactggtt tttgttgtt tttgttttt tatatgtaaa 2460
356 ataaaaatag tgaaaggag 2479
359 <210> SEQ ID NO: 11
360 <211> LENGTH: 475
361 <212> TYPE: DNA
362 <213> ORGANISM: Homo sapiens
364 <220> FEATURE:
367 <400> SEQUENCE: 11
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370 acggtggccg tgggcacccg cggggcgcg cggcgggggc cgctggcccg cggcggcg 120
372 ggcataagg tcacgtcgct cgacggcg cagctgcgca agatgctccg caaggaggcg 180
374 ggcgcgcgct gcgtggtgct cgactgcg ccttatcttg ccttcgctgc ctgaacgtg 240
376 cgcggtcgc tcaacgtcaa cctcaactcg gtggtgctgc ggcggggccc gggcggcg 300
378 gtgtcggcgc gctacgtgct ggaccagggc agccgccact ggcagaagct gcgagaggag 360
380 agcgcgcgc gtgtcgtcct caccctgcta ctgcttgcc taccgcgccc cccgcgggtc 420
382 tacttctca aaggtgagcg ctcggggtcc ctgccacgct cgcctctccg gcgcc 475
385 <210> SEQ ID NO: 12
386 <211> LENGTH: 20
387 <212> TYPE: DNA
388 <213> ORGANISM: Artificial Sequence
390 <220> FEATURE:
392 <223> OTHER INFORMATION: Antisense Oligonucleotide
394 <400> SEQUENCE: 12
395 gacgtgacct tcatgccgcc 20
398 <210> SEQ ID NO: 13
399 <211> LENGTH: 20

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VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:152 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3